CLAIM AMENDMENTS

1.-41. (Cancelled)

42. (Currently Amended) ~~Method~~ A method for the detection of *L. brevis* ~~a microorganism relevant to brewing~~ in a sample, which comprises the following steps:

(a) bringing the sample into contact with a combination of at least two first nucleic acid molecules (primers), which hybridize with a region of a ~~microbial~~ *L. brevis* nucleic acid ~~conserved in microorganisms relevant to brewing;~~, wherein each of the at least two first nucleic acid molecules are selected from the group consisting of:

(i) a nucleic acid sequence consisting of SEQ ID NO 1, 21, 73 or 74,or a fragment thereof comprising at least 10 nucleotides,

(ii) a nucleic acid which specifically hybridizes with a nucleic acid according to (i),

(iii) a nucleic acid which is at least 70% identical with a nucleic acid according to (i) or (ii), and

(iv) a nucleic acid which is complementary to a nucleic acid according to (i)-(iii),

(b) ~~amplification of~~ amplifying the ~~microbial~~ *L. brevis* nucleic acid or a portion thereof to produce at least one amplification fragment;

(c) ~~bringing~~ contacting the amplification fragments obtained in step (b) ~~into contact~~ with at least one second nucleic acid molecule (probe), which specifically hybridizes with at least one amplification fragment that comprises a sequence of the microbial nucleic acid specific for *L. brevis*, wherein the at least one second nucleic acid molecule is selected from the group consisting of:

(i) a nucleic acid sequence consisting of SEQ ID NO 1, 21, 73 or 74, or a fragment thereof comprising at least 10 nucleotides,

(ii) a nucleic acid which specifically hybridizes with a nucleic acid according to (i),

(iii) a nucleic acid which is at least 70% identical with a nucleic acid according to (i) or (ii), and

(iv) a nucleic acid which is complementary to a nucleic acid according to (i)-(iii), ~~all microorganisms relevant to brewing or for one or several families, genera or species of microorganisms relevant to brewing~~; and

(d) ~~detection of~~ detecting at least one hybrid nucleic acid which consists of an amplification fragment and a second nucleic acid molecule introduced in step (c), whereupon ~~a microorganism relevant to brewing~~ *L. brevis* is detected in a sample.

43.-49. (Cancelled)

50. (Currently Amended) ~~Method~~ The method according to Claim 42, characterized in that the amplification comprises a polymerase chain reaction (PCR).

51. (Currently Amended) ~~Method~~ The method according to Claim 42, characterized in that the amplification comprises a ligase chain reaction.

52. (Currently Amended) ~~Method~~ The method according to Claim 42, characterized in that the amplification comprises an isothermal nucleic acid amplification.

53. (Currently Amended) ~~Method~~ The method according to Claim 42, characterized in that the second nucleic acid molecule is modified or labeled to produce a detectable signal, wherein the modification or label ~~labeling being selected~~ is selected from the group consisting of (i) radioactive groups, (ii) colored groups, (iii) fluorescent groups, (iv) groups for immobilization on a solid phase and (v) groups which allow an indirect or direct reaction~~, particularly~~ by means of antibodies, antigens, enzymes and/or substances with affinity for enzymes or enzyme complexes.

54. (Currently Amended) ~~Method~~ The method according to Claim 42, characterized in that the first nucleic acid molecule and/or the second nucleic acid molecule are at least 10 nucleotides long.

55. (Currently Amended) ~~Method~~ The method according to Claim 54, characterized in that the first nucleic acid molecule and/or the second nucleic acid molecule are ~~at least~~ 15-30 nucleotides long.

56. (Currently Amended) ~~Method~~ The method according to Claim 42, characterized in that the first nucleic acid molecule and/or the second nucleic acid molecule is modified ~~in~~ such that up to 20% of the nucleotides in the 10 consecutive nucleotides are replaced by nucleotides which do not naturally occur in bacteria.

57.-63. (Cancelled)

64. (New) A method for the detection of *L. brevis* in a sample, which comprises the following steps:

(a) bringing the sample into contact with a combination of at least two first nucleic acid molecules (primers), which hybridize with a region of a *L. brevis* nucleic acid, wherein each of the at least two first nucleic acid molecules are selected from the group consisting of:

(i) a nucleic acid sequence consisting of SEQ ID NO 1, 21, 73 or 74, or a fragment thereof comprising at least 10 nucleotides,

(ii) a nucleic acid which specifically hybridizes with a nucleic acid according to (i),

(iii) a nucleic acid which is at least 90%, identical with a nucleic acid according to (i) or (ii), and

(iv) a nucleic acid which is complementary to a nucleic acid according to (i) to (iii),

(b) amplifying the *L. brevis* nucleic acid or a portion thereof to produce at least one amplification fragment;

(c) contacting the amplification fragments obtained in step (b) with at least one second nucleic acid molecule (probe), which specifically hybridizes with at least one amplification fragment, wherein the at least one second nucleic acid molecule is selected from the group consisting of:

(i) a nucleic acid sequence consisting of SEQ ID NO 1, 21, 73 or 74, or a fragment thereof comprising at least 10 nucleotides,

(ii) a nucleic acid which specifically hybridizes with a nucleic acid according to (i),

(iii) a nucleic acid which is at least 90% identical with a nucleic acid according to (i) or (ii), and

(iv) a nucleic acid which is complementary to a nucleic acid according to (i)-(iii), and

(d) detecting at least one hybrid nucleic acid which consists of an amplification fragment and the second nucleic acid molecule introduced in step (c).